Supplementary Table 2. Chi-square tests for distribution of genotypes between control and heart failure (HF) patients.

GENE/location	SNP	Genotype Counts						Chi-square *P*-value
		Control Subjects			HF Patients			
		11	**12**	**22**	**11**	**12**	**22**	
FAM19A	rs10506410	22	155	194	76	532	847	0.1206
TRIM38	rs10947055	5	68	375	16	248	1286	0.9074
ESRRG	rs12757165	195	204	47	621	563	121	0.3443
C15orf54	rs12907914	76	219	154	236	715	576	0.3955
COL17A1	rs1320448	0	6	443	0	25	1508	0.8212
NRG3	rs1484170	21	129	298	46	448	1004	0.2497
FGF1	rs152528	170	199	70	549	680	251	0.7881
HTR2A	rs1575891	24	156	249	87	576	827	0.6451
SLCA1	rs16830359	0	5	446	1	18	1518	0.8582
PLXNA2	rs17259784	17	123	306	48	443	1025	0.6682
UBE3A	rs17636733	114	220	109	461	734	341	0.1928
ZWINT	rs1916521	63	213	167	192	729	600	0.6233
PHF11	rs2031532	194	196	58	580	566	167	0.9498
20p12*	rs2207418	36	174	242	221	576	750	0.0016
RAF1	rs3729931	167	235	45	612	738	169	0.3306
SOX4	rs4236016	0	2	446	1	5	1530	0.8043
GRIK2	rs4520040	1	29	426	5	120	1412	0.5463
GRM7	rs4686148	43	190	199	115	680	705	0.3097
KCNIP4	rs6817687	293	128	13	967	469	49	0.6503
CA8	rs6995588	447	10	1	1527	29	2	0.8235
DPPA4	rs769554	438	3	0	1460	15	0	0.7175

*, $p < 0.05$ for allele difference; homozygous GG unadjusted RR = 1.98 (95% CI = 1.35 to 2.90, $p = 0.0004$); adjusted RR = 1.85 (95% CI = 1.25 to 2.73, $p = 0.0019$)